

SEQUENCE LISTING

<110> BAYER AG

<120> Use of VLCFAE for identifying herbicidally active compounds

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<170> PatentIn Ver. 2.1

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<213> Arabidopsis thaliana

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<222> (1119)..(1745)

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<222> (1821)..(2438)

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178

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226
Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn Arg
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274
Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser Val
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322
Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu Lys
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370
Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr Leu
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418
Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly Ser
70 75 80

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466
Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu Ala
85 90 95

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514
Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val Tyr
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Lys Pro Ser Asp Glu His Lys
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Val Thr Lys Glu Glu Phe Ile Glu Leu
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Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys Lys
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Ser Ile Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg Glu		
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1337		
Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu Lys		
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1385		
Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys Ser		
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Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly Tyr		
275	280	285
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310	315	320
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Ala Ala Asp Asp Arg Ser Phe Arg		
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Ser Val Tyr Gln		
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1880		

Glu Glu Asp Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu
350 355 360 365

atg gaa gtt gga ggt gaa gct ctc aag aca aac atc act acc tta ggt
1928

Met Glu Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly
370 375 380

cct ctt gtc cta cct ttc tcc gag cag ctt ctc ttc ttt gct gct ttg
1976

Pro Leu Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu
385 390 395

ctc cgc cga aca ttc tca cct gct gcc aaa acg tcc aca acc act tcc
2024

Leu Arg Arg Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Ser
400 405 410

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2072

Phe Ser Thr Ser Ala Thr Ala Lys Thr Asn Gly Ile Lys Ser Ser Ser
415 420 425

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2120

Ser Asp Leu Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu
430 435 440 445

cat ttt tgc ttc cac gcg gca agc aaa gta gtg ctt gaa gag ctt caa
2168

His Phe Cys Phe His Ala Ala Ser Lys Val Val Leu Glu Glu Leu Gln
450 455 460

aag aat cta ggc ttg agt gaa gag aat atg gag gct tct agg atg aca
2216

Lys Asn Leu Gly Leu Ser Glu Glu Asn Met Glu Ala Ser Arg Met Thr
465 470 475

ctt cac agg ttt gga aac act tct agc agt gga atc tgg tat gag ttg
2264

Leu His Arg Phe Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu
480 485 490

gct tac atg gag gcc aag gaa agt gtt cgt aga ggc gat agg gtt tgg
2312

Ala Tyr Met Glu Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp
495 500 505

cag atc gct ttc ggt tct ggt ttt aag tgt aac agt gtg gtg tgg aag
2360

Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys
510 515 520 525

gca atg agg aag gtg aag aag cca acc agg aac aat cct tgg gtg gat
2408

Ala Met Arg Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp
530 535 540

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2458

Cys Ile Asn Arg Tyr Pro Val Pro Leu
545 550

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2578

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2638

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35 40 45

Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
50 55 60

Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
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Ser Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu
85 90 95 -

Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val
100 105 110

Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
115 120 125

Tyr Lys Pro Ser Asp Glu His Lys Val Thr Lys Glu Glu Phe Ile Glu
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Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys
145 150 155 160

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195 200 205

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225 230 235 240

Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
245 250 255

Cys Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp Met Leu Gln
260 265 270

Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly
275 280 285

Tyr Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys
290 295 300

Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg
305 310 315 320

Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His
325 330 335

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340 345 350

Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu Val
355 360 365

Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val
370 375 380

Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Leu Arg Arg
385 390 395 400

Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Ser Phe Ser Thr
405 410 415

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Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys
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485 490 495

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Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg
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Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp Cys Ile Asn
530 535 540

Le A 34 730-Foreign Countries

- 7 -

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545 550